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Glu Met Gln Cys Met Trp Phe Gln Thr Glu Cys Ala Gln Ala Tyr Lys  
 210 215 220  
 Ala Met Asn Lys Phe Gly Glu Ala Leu Lys Lys Cys His Glu Ile Glu  
 225 230 235 240  
 Arg His Phe Ile Glu Ile Thr Asp Asp Gln Phe Asp Phe His Thr Tyr  
 245 250 255  
 Cys Met Arg Lys Ile Thr Leu Arg Ser Tyr Val Asp Leu Leu Lys Leu  
 260 265 270  
 Glu Asp Val Leu Arg Gln His Pro Phe Tyr Phe Lys Ala Ala Arg Ile  
 275 280 285  
 Ala Ile Glu Ile Tyr Leu Lys Leu His Asp Asn Pro Leu Thr Asp Glu  
 290 295 300  
 Asn Lys Glu His Glu Ala Asp Thr Ala Asn Met Ser Asp Lys Glu Leu  
 305 310 315 320  
 Lys Lys Leu Arg Asn Lys Gln Arg Arg Ala Gln Lys Lys Ala Gln Ile  
 325 330 335  
 Glu Glu Glu Lys Lys Asn Ala Glu Lys Glu Lys Pro Gln Arg Asn Pro  
 340 345 350  
 Lys Lys Lys Lys Asp Asp Asp Asp Glu Glu Ile Gly Gly Pro Lys Glu  
 355 360 365  
 Glu Leu Ile Pro Glu Lys Leu Ala Lys Val Glu Thr Pro Leu Glu Glu  
 370 375 380  
 Ala Ile Lys Phe Leu Thr Pro Leu Lys Asn Leu Val Lys Asn Lys Ile  
 385 390 395 400  
 Glu Thr His Leu Phe Ala Phe Glu Ile Tyr Phe Arg Lys Glu Lys Phe  
 405 410 415  
 Leu Leu Met Leu Gln Ser Val Lys Arg Ala Phe Ala Ile Asp Ser Ser  
 420 425 430  
 His Pro Trp Leu His Glu Cys Met Ile Arg Leu Phe His Ser Val Cys  
 435 440 445  
 Glu Ser Lys Asp Leu Pro Glu Thr Val Arg Thr Val Leu Lys Gln Glu  
 450 455 460  
 Met Asn Arg Leu Phe Gly Ala Thr Asn Pro Lys Asn Phe Asn Glu Thr  
 465 470 475 480  
 Phe Leu Lys Arg Asn Ser Asp Ser Leu Pro His Arg Leu Ser Ala Ala  
 485 490 495  
 Lys Met Val Tyr Tyr Leu Asp Ser Ser Ser Gln Lys Arg Ala Ile Glu  
 500 505 510  
 Leu Ala Thr Thr Leu Asp Gly Ser Leu Thr Asn Arg Asn Leu Gln Thr



TCTATAAGCA	TGCTGGGAAT	ATTAAAGAAG	CTGCCAGGTG	GATGGATGAA	GCCCAGGCC	900
TGGACACAGC	AGACAGATTT	ATTAATTCCA	AGTGTGCAAA	ATACATGTTA	AAAGCCAACC	960
TGATTAAAGA	GGCTGAAGAA	ATGTGTTCCA	AGTTTACGAG	GGAAGGAACT	TCAGCGGTAG	1020
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AAATCACCGA	TGACCAGTTT	GACTTTCATA	CATACTGTAT	GAGGAAGATC	ACCCCTTAGAT	1200
CATATGTGGA	CTTATTAAAA	CTAGAAGATG	TACTTCGACA	GCATCCATTT	TACTTCAAAG	1260
CAGCGAGAAT	TGCTATTGAG	ATCTATTGGA	AGCTTCATGA	CAACCCTCTG	ACAGATGAGA	1320
ACAAAGAACA	CGAGGCTGAT	ACAGCAAACA	TGTCTGACAA	AGAGCTAAAG	AAACTGCGTA	1380
ATAAACAAAG	AAGAGCTCAA	AAGAAAGCCC	AGATTGAAGA	AGAGAAAAAA	AATGCCGAAA	1440
AAGAAAAGCC	GCAACGGAAT	CCGAAAAAGA	AAAAGGATGA	TGATGACGAA	GAAATTGGAG	1500
GCCCCAAAGA	AGAGCTTATC	CCTGAGAAAC	TGGCCAAGGT	TGAAACTCCA	TTGGAAGAAG	1560
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GGGCATTTGC	TATTGATTCT	AGTCATCCCT	GGCTTCATGA	GTGCATGATT	CGACTCTTTC	1740
ATTCTGTGTG	TGAAAGTAAA	GACTTACCCG	AAACAGTTAG	AACAGTATTA	AAACAAGAAA	1800
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CTAGTCAAAA	ACGAGCAATA	GAGCTGGCGA	CAACACTTGA	TGGATCCCTC	ACCAACAGAA	1980
ACCTTCAGAC	TTGCATGGAA	GTGTTGGAAG	CCTTGTGTGA	TGGTAGCCTA	CGAGACTGTA	2040
AAGAAGCTGC	CGAAGCCTAC	AGAGCAAGTT	GTCATAAGCT	TTTCCCTTAT	GCTTTGGCTT	2100
TCATGCCTCC	TGGATACGAA	GAGGATATGA	AGATCACAGT	GAACGGAGAT	AGTTCTGCAG	2160
AAACGGAAGA	ACTGGCCAAT	GAAATCTGAA	CATCATTTAA	CAAGCAAATG	GAATGACTTT	2220
GGACCATATC	TAGTGATATA	TATTTTTGTC	ACGCACCTGC	TGCATTGCTC	TTACTTACAC	2280
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GTGTGGCAGA	AATATTACTT	TAAATTTGTC	TTGTGAGATT	TTGCTATATC	TCAGACAGCA	2580
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TAGCATCTGC	CTGATTCTGT	TACGGGGTTG	GTGATTGACC	ATAGGAAGTA	TGCAATGTGA	2700
ATCACTGTGT	ACAGAGCCGT	CTACAACACA	TGCTTGACGT	TGTAGAGACT	GGGACACATA	2760
GCTACCAAGC	GGATTAAAGT	AAACCTAGAA	GGTGTTCAGT	ACGTGTGTTG	TGTTTCCAAA	2820

ATTCACGTGA CATGATCAGT TTGGTGTCT TGTACCACAG TTTTAAACCG AAGGAACCAG	2880
TTGGAACAAT CTCAATTTAA CTAAACTTG AAGAACTAAA ATAACAATGC AAACCTTTAT	2940
CATTGTTTTG GCCAAACTTG TTAAACTGT AATGCAAGAA CCAAATGCAC TGTGATGTGG	3000
CACCAACTAA TTATGCAAGC ATGAATTTTT CACCTGAGAG TGAAAAAGA AAACTCTACC	3060
ATGGCTTGAA GTTACAGGAG CAGAACTCCT GACTACCATT CTATGACTGA TGAAGAGACT	3120
AATATCTAAA ACCTCAGCAG GCCTTGTTCA CGATATGCAG AAAAAGTGCT GCAGTTTAGA	3180
TACCTCTGGG AACTTTTCCA CAGTGCACA GGTGTGTAAT ACTTGAAGCC CTTCAATTTCT	3240
AAGAATATAT TTCTCGCTCA GTTGTTCAG GCAAGCCCAA GACTTTGTAA TTTTAAAGG	3300
GCCCAAGATT TTTTTTCAA TAACAGACCA GCTTCTTTT CCTGCAGTTA CAAATGTAAT	3360
TTCTTTTTTT TTTTGTGTG AAACATAAGG TACCAAATAT GCAATAAATT GTTTTGGG	3418

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 1413 base pairs

(B) TYPE: cDNA

(C) STRANDEDNESS: both

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTISENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCTGGGCTTT CTTTGAGCT CTTCTTGTT TATTACGAG TTTCTTAGC TCTTTGTCAG	60
ACATGTTTGC TGTATCAGCC TCGTGTCTT TGTTCATC TGTGAGAGG TTGTCATGAA	120
GCTTCAAATA GATCTCAATA GCAATTCTCG CTGCTTTGAA GTAAATGGA TGCTGTCGAA	180
GTACATCTTC TAGTTTAAAT AAGTCCACAT ATGATCTAAG GGTGATCTTC CTCATACAGT	240
ATGTATGAAA GTCAAAGTGG TCATCGGTGA TTTCTATAAA ATGTCTCTCA ATTTTCATGAC	300
ATTTCTTAAG TGCTTCACCA AATTTGTTCA TTGCTTTGTA TGCCTGAGCA CACTCTGTCT	360
GGAACCACAT AACTGCATT TCATTCAGGT TCTCTACCGC TGAAGTTCCT TCCCTCGTAA	420
ACTTGGAACA CATTTCTTCA GCCTCTTAA TCAGGTGGC TTTTAACATG TATTTTGCAC	480
ACTTGGAATT AATAATCTG TCTGCTGTGT CCAGGGCCTG GGCTTCATCC ATCCACCTGG	540
CAGCTTCTTT AATATCCCA GCATGCTTAT AGATTTTAGC TTTTACAAGA AAGAGTTCTA	600
TCAATGTTGG TGTACTTCA ATTGCAGTAT TTATGTATC CAGAGCAATG GATGGCTGAC	660
CAATTTTATC ATAATGCTGT GCCAAATAGT ACTGGACCCA AAGTAATGTG GTTGGAGGTT	720

CCTCCTTTCC ATCATCATTG GGGTTAAATA GCGACAAC TTTTAGAGAA GTTTCATAAC 780  
CAACTACTAG TTCTTCTACG ATTGCCACCT TCTCTTTATC TCTGTATAAA GACCTCAAGG 840  
TATTGAAGAC AGGTGGACAG CCCTTGCTGA AATTCATCCT TAGGAACCTA TCCAAACACT 900  
CCTTAAACTT CTCTCCAGAT AAAAAGTTTA AGGGCAGCTT TCTTGGCACG AGTCCCCTGG 960  
GGTATTTAGT CCAGGCTTCC TCATATATTT TTAGCCGTTT TAACATATTA GCTGGCTTCA 1020  
GTGCTTTTTT TAAGCCTTTG TAATAGGCCC AATTTTCAGG ATTCTCTCTT TGTAATCCTC 1080  
TATAAACGTC AGCAGCATCT TCCAAACGAC ACAACTGCAA CAGAAGTTCC CCTTTGGTTT 1140  
CTTCAACAGC AAGTTTATCA CAAATCTGCT TTTCATAGGT ACAAAGATGT TCCAGGGCTT 1200  
CTCTATAAAG ACCTGCTTCC CGAAGAACTT GATTCTGATA TAAGAGGAGT TCACTATATT 1260  
CATAATCCAC TTTATCAGGA GATGTCTGCT GTGTTTTCTT AACTCTTCT AAAATTTTTG 1320  
CTGCCATTTT ATAGTCTTCT AATAAATGGT AAAGCATAAC CAATCCATGA TGCTCACTCT 1380  
GCAGATCCTC TATCATCTTG CGGGTGTTAC TTG 1413

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 3418 base pairs

(B) TYPE: cDNA

(C) STRANDEDNESS: both

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTISENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CCCAAAACAA TTTATTGCAT ATTTGGTACC TTATGTTTGA CAACAAAAAA AAAAAGAAAT 60  
TACATTTGTA ACTGCAGGAA AAAGAAGCTG GTCTGTTATT GAAAAAATAA TCTTGGGCCC 120  
TTTAAAAATT ACAAAGTCTT GGGCTTGCCT GAAACAACCTG AGCGAGAAAT ATATTCTTAG 180  
AAATGAAGGG CTTCAAGTAT TACAAACCTG TGACACTGTG GAAAAGTTCC CAGAGGTATC 240  
TAAACTGCAG CACTTTTTCT GCATATCGTG AACAAGGCCT GCTGAGGTTT TAGATATTAG 300  
TCTCTTCATC AGTCATAGAA TGGTAGTCAG GAGTTCTGCT CCTGTAACCT CAAGCCATGG 360  
TAGAGTTTTT TTTTTTCACT CTCAGGTGAA AAATTCATGC TTGCATAATT AGTTGGTGCC 420  
ACATCACAGT GCATTTGGTT CTTGCATTAC AGTTTAAACA AGTTTGGCCA AAACAATGAT 480  
AAAGGTTTGC ATTGTTATTT TAGTCTTCA AGTTTGTAGT AAATTGAGAT TGTTCACACT 540  
GGTTCCTTCG GTTAAAAACT GTGGTACAAG AACACCAAC TGATCATGTA CAGTGAATTT 600

TGGAACACA ACACACGTAC TGAACACCTT CTAGGTTTCA CTTAATCCGC TTGGTAGCTA	660
TGTGTCCCAG TCTCTACAAC GTCAAGCATG TGTGTAGAC GGCTCTGTAC ACAGTGATTG	720
ACATTGCATA CTTCTATGG TCAATCACCA ACCCCGTAAC AGAATCAGGC AGATGCTAAA	780
GCCCCAACAA CTCTTTGTGC TCAGTGAAAG AATCCAGTGC TAAAACAGCA TTTATTTATG	840
CTGTCTGAGA TATAGCAAAA TCTCACAAGA CAAATTTAAA GTAATATTTT TGCCACACAC	900
CTGCTATGTT AGCTGTTATA GCCTCCAGAT TTTATATAAA TTAGTTAAAA ACATGGGAAG	960
GGAAGGTAGG AATAGGATAC GGATTTTTTT TTCTTTTAAA CCCCTCAATT TTAGCAGCTT	1020
TTAATTTTTT AAGAACTGA ACCTATATCC TGTAATGTTA GATATTTTAT ATATAGTTTT	1080
CAGCAGGATA AAAAACGTAA GACTATTTGA AGGCAAGAAC ATTTACTCCT CTCATTCTGT	1140
GTAAGTAAGA GCAATGCAGC AGGTGCGTGA CAAAAATATT ATACACTAGA TATGGTCCAA	1200
AGTCATTCCA TTGCTTGTT TAATGATGTT CAGATTTTCA TGGCCAGTTC TTCCGTTTCT	1260
GCAGAACTAT CTCCGTTTAC TGTGATCTTC ATATCCTCTT CGTATCCAGG AGGCATGAAA	1320
GCCAAAGCAT AAGGGAAAAG CTTATGACAA CTTGCTCTGT AGGCTTCGGC AGCTTCTTTA	1380
CAGTCTCGTA GGCTACCATC ACACAAGGCT TCCAACACTT CCATGCAAGT CTGAAGGTTT	1440
CTGTTGGTGA GGGATCCATC AAGTGTGTG GCCAGCTCTA TTGCTCGTTT TTGACTAGAA	1500
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CCAATTTCTT CGTCATCATC ATCCTTTTTT TTTTTCGGAT TCCGTTGCGG CTTTTCTTTT	1980
TCGGCATTTC TTTTCTCTTC TTCAATCTGG GCTTTCCTTT GAGCTCTTCT TTGTTTATTA	2040
CGCAGTTTCT TTAGCTCTTT GTCAGACATG TTTGCTGTAT CAGCCTCGTG TTCTTTGTTC	2100
TCATCTGTCA GAGGGTTGTC ATGAAGCTTC AAATAGATCT CAATAGCAAT TCTCGCTGCT	2160
TTGAAGTAAA ATGGATGCTG TCGAAGTACA TCTTCTAGTT TTAATAAGTC CACATATGAT	2220
CTAAGGGTGA TCTTCCTCAT ACAGTATGTA TGAAAGTCAA ACTGGTCATC GGTGATTCTT	2280
ATAAAATGTC TCTCAATTTT ATGACATTTT TTAAGTGCTT CACCAAATTT GTTCATTGCT	2340
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TGCAACAGAA GTTCCCCTTT GGTTCCTTCA ACAGCAAGTT TATCACAAAT CTGCTTTTCA	3180
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ATAACCAATC CATGATGCTC ACTCTGCAGA TCCTCTATCA TCTTGCGGGT GTTACTTG	3418